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NEMATODE JH-LIKE SEQUENCES

1
caa gtt tga gat att taa att att att ttg gtg cta aga aaa att ttg tga aaa ATG AAT
M N

61
TAT TCA AAG GAT GCC CCA GAA TTT GTT GTG TCT CCA AAA GAT GCA CGC GAA TTT GTT GTA
Y S K D A P E F V V S P K D A R E F V V

121
AAA TGT ATG CAA ACA GTT GGA ACA TCC CCT GAC CAT GCT GGT CAA TTA GCA GAT CTA TTA
K C M Q T V G T S P D H A G Q L A D L L

181
TTG GAT GCT GAT CTT GTT GGA CAC TAT AGT CAT GGT CTA AAT CGA CTT CAT ATT TAT GTG
L D A D L V G H Y S H G L N R L H I Y V

241
GAT GAC GTC AAA AAC GGA GTT AAA GGA AAT GGA GTT CCA AAA GTG TTA AAA CAA AAA GGA
D D V K N G V K G N G V P K V L K Q K G

301
GGC ACT GCT TGG GTT GAT GGA GAA AAT CTT CTG GGT GCA GTT GTT GGA AAC TTC TGT ACC
G T A W V D G E N L L G A V V G N F C T

361
GAC TTG GCT ATT AAA TTG GCT AAA GAA TTT GGC GTT GCT TGG GTG GTA ACA AAA AAT TCT
D L A I K L A K E F G V A W V V T K N S

421
AAT CAT TAT GGA GCT TGT CAA CAT TAT ACT AAG AAA ATT GCA AAT GCA GGA ATG GTG GGA
N H Y G A C Q H Y T K K I A N A G M V G

481
ATG TCT TTT ACA AAT ACA TCG CCT CTC ATG TTC CCC TGC CGA TCT TCT GAG ATT GGA CTT
M S F T N T S P L M F P C R S S E I G L

541
GGT ACA AAC CCT CTT TCT TGT TGT GTC AAC TCG GAA AAG ACA GGA GAC AGT TTT TTG TTA
G T N P L S C C V N S E K T G D S F L L

601
GAC ATG GCT ACG ACA ACT GTT GCT CTT GGA AAG GTA GAG CTG GCA GAT TGT CGC GGT AAA
D M A T T T V A L G K V E L A D C R G K

661
ACA CAA ATT CCC TCC ACA TGG GGT GCC GAT TCT AAA GGC AAT CCA TCG ACT GAT ACA CAA
T Q I P S T W G A D S K G N P S T D T Q

721
GTT GTT TTA CAC GGT GGC GGA CTT TTG CCT TTA GGC GGT ATA GAA GAG ACG GGA TCT TAC
V V L H G G G L L P L G G I E E T G S Y

781
AAA GGA ACG GGT CTT TCA ATG ATG GGT GAA TTG TTT TGT GGA ATT TTG GCA GGG TCA AGT
K G T G L S M M G E L F C G I L A G S S

841
TTT GGA AAA AAT GTA CGA TTA TGG GGG CAA TCA CAC AAA GCC GCT GAC AAT GGC CAA TGT
F G K N V R L W G Q S H K A A D N G Q C

901
TTT GTT GCT ATT GAT CAA GAA TGT TTT GCC CCA GGA TTT GCT CCT CGT TTA CAA CAA TTT
F V A I D Q E C F A P G F A P R L Q Q F

961
TTG GAT GAA ACA CGG AAT TTG AAA CCG ATT TCT GAA GAA AAG CCT GTT CTA GTG CCT GGA
L D E T R N L K P I S E E K P V L V P G

1021
GAT CCT GAA AGA ATG AAT ACA GAA TAT AGC CAA AAG GCT GGA GGT TTG GTA TAC CAA GAA
D P E R M N T E Y S Q K A G G L V Y Q E

1081
GGG CAG ATA AAA GCT TTG GAA GAG TTG GCC ACA AAA TGT GAT GTT CAA ATG TTC TCA TAC
G Q I K A L E E L A T K C D V Q M F S Y

1141
AAA CGA CTA AAA tga gga tga gat tta aat att ttt ttg tgt agc tga aac tga ctt caa
K R L K *

1201
acg aga aat gaa caa ttt cct aaa aag cag tta gat aag ggt tta ttt ttc att tat tta

1261
ttt ttt aac ctc att ttt tat ata cga ata aaa tta atg ctc *aa aaa aaa aaa aaa

1321
aaa aaa a

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FIGURE 1

1
tgg tgc taa gaa aaa ttt tgt gcg aaa ATG AAT TAT TCA AAG GAT GCC CCA GAA TTT GTT
M N Y S K D A P E F V
61
GTC TCT CCA AAA GAT GCT CGC GAA TTT GTT GTA AAA TGT ATG CAA ACA GTT GGA ACA TCC
V S P K D A R E F V V K C M Q T V G T S
121
CCT GAC CAT GCT GGT CAA TTA GCA GAT CTC TTA TTA GAT GCT GAT CTT GTT GGG CAT TAC
P D H A G Q L A D L L L D A D L V G H Y
181
AGT CAT GGT CTA AAT CGG CTT CAT ATT TAT GTG GAT GAC GTC AAA AAT GGA GTT AAA GGA
S H G L N R L H I Y V D D V K N G V K G
241
AAT GGA GTT CCA AAA GTG TTA AAA CAA AAA GGA GGC ACT GCT TGG GTG GAT GGA GAA AAT
N G V P K V L K Q K G G T A W V D G E N
301
CTT TTG GGT GCA GTT GTT GGC AAC TTC TGT ACC GAT TTG GCT ATT AAA TTG GCT AAA GAA
L L G A V V G N F C T D L A I K L A K E
361
TTT GGT GTT GCT TGG GTG GTA ACA AAA AAT TCT AAT CAT TAT GGA GCT *GT CAA CAT TAT
F G V A W V V T K N S N H Y G A X Q H Y
421
ACT AAG AAA ATT GCG AAT GCA GGA ATG GTG GGA ATG TCA TTT ACA AAT ACT TCA CTT CTC
T K K I A N A G M V G M S F T N T S P L
481
ATG TTC CCC TGC CGT TCT TCT GAG ATC GGA CTA GGC ACA AAC CCT CTT TCT TGT TGT GCC
M F P C R S S E I G L G T N P L S C C A
541
AAC TCG GAA AAG ACA GAA GAC AGT TTT TTG TTA GAC ATG GCT ACT ACA ACT GTT GCT CTA
N S E K T E D S F L L D M A T T T V A L
601
GGA AAG GTT GAG CTG GCA AAT TGT CGC GGT AAA ACA CAA ATT CCC TCA GCA TGG GGT GCC
G K V E L A N C R G K T Q I P S A W G A
661
GAT TCT AAA GGC AAT CCA TCA ACA GAC ACA CAA GTT GTT TTA CAT GGT GGC GGA CTT TTG
D S K G N P S T D T Q V V L H G G G L L
721
CCT TTA GGC GGT ATA GAA GAG ACG GGA TCT TAC AAA GGA ACG GGT CTC TCA ATG ATG GGT
P L G G I E E T G S Y K G T G L S M M G
781
GAA TTG TTT TGT GGA ATT TTG GCA GGG TCA AGT TTT GGA AAA AAT GTA CGA TTA TGG GGG
E L F C G I L A G S S F G K N V R L W G
841
CAA TCA CAC AAA GCC GCT GAC AAT GGC CAA TGT TTT GTT GCT ATT GAT CAA GAA TGT TTT
Q S H K A A D N G Q C F V A I D Q E C F
901
GCC CCA GGA TTT GCT CCT CGT TTA CAA CAA TTT TTG GAT GAA ACA CGG AAT TTG AAA CCG
A P G F A P R L Q Q F L D E T R N L K P
961
ATT TCT GAA GAA AAG CCT GTT CTA GTG CCT GGA GAT CCT GAA AGA ATG AAT ACA GAA TAT
I S E E K P V L V P G D P E R M N T E Y
1021
AGC CAA AAG GCT GGA GGT TTG GTA TAC CAA GAA GGG CAG ATA AAA GCT TTG GAA GAG TTG
S Q K A G G L V Y Q E G Q I K A L E E L
1081
GCC ACA AAA TGT GAT GTT CAA ATG TTC TCA TAC AAA CGA CTA AAA TGA gga tga gat tta
A T K C D V Q M F S Y K R L K *
1141
aat att ttt ttg tgt agc tga aac tga ctt caa acg aga aat gaa caa ttt cct aaa aag
1201
cag tta gat aag ggt tta ttt ttc att tat tta ttt ttt aac ctc att ttt tat ata cga
1261
agc aga tat gac tga aac tgg agg tgg tga ttc tgt tga atc tgc aag tgt tta tgc taa

FIGURE 2A

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1321
ctc tgt ttg tga aat gtg cgg aaa tta tga ggt tca act tca aac aat tca aag cag tca

1381
gga tac tct cag gga gaa att ggc agc tgc taa aga att gta tga gaa ata tgg caa gga

1441
att gac aga aga gag gca tta tcg aaa gga att gga aat taa att tgc tgc ttt aaa tga

1501
aga aac tga agg gaa aat tca gca atg tat tac caa tac aga aga ctt tga cag cgt att

1561
gcc ttc tca gta aaa aac aa* aag ctg att tgt ctg ttt tgg aat c*c aat tag aat tgg

1621
cta gga atc gtc aaa aag agc ttc aag aac aat tgg ttt tgt taa atg aaa ggt atg aaa

1681
aac ttt tac att taa aat ctc aat gtg ctg aag aaa tgc gtg aac aac aaa ttg aac tgc

1721
ctc aaa cag ttg aag aac ttc aat ttt tgg cat tgc agt tga *ag agg aat tga taa ctg

1781
aac gtg cag cac gtg agc atg aaa gga ggg aat taa atg atg aat tgg cta tgg cac gtc

1841
aac agc ttg ttg aat tgg aaa ttt gtc c*a gag aaa atg aag aat gaa ttt tat gat ata

1901
taa aaa tat att tat ttt gct caa ata g*t ttt ata aat ttt aag agc tga tag aaa aat

1961
tta gtt ttg *aa ttt ttg aag aat ata ttt t*t acg gtt tgc ac* cct tag aat ggt ttt

2021
gtt tta ata aat gc* c*g gtt gg* aaa aaa aaa aaa aaa aaa aaa

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Amino acid alignment

1 *M. incognita* MDH1

2 *M. incognita* MDH2

3 *C. elegans* MDH1

4 *C. elegans* MDH2

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      10      20      30      40      50      60
1  .....MNYSDAPFVVSPKDAREFVVK: 23
2  .....MNYSDAPFVVSPKDAREFVVK: 23
3  .....MTIKDKREFNETDEIVISKEKLDSEVLE: 28
4  MNLQRALVFTGGHISRYQAVIAVNSVGKNARYSTTDDNMAAPEESVVAKDEMKRIMVE: 60

      70      80      90     100     110     120
1  CMQTVGTSPDHAGQLADLLDADLVGHYSHGLNRLHIYVDDVKNG VKNGGVPEKVLKQKG: 82
2  CMQTVGTSPDHAGQLADLLDADLVGHYSHGLNRLHIYVDDVKNG VKNGGVPEKVLKQKG: 82
3  CFAKAGCTGDHAQQLAETLLCSDYRGHYSHGIERLHIYVDDLMKSTAVTGTTPQVLKSKG: 88
4  CMTKVGATESHATQLALVLLGDIRGHYSHGLNRLDMYVRDIEQNVCKGDGEPILKEKA:120

     130     140     150     160     170     180
1  GTAWVDGEMLLGAVVGHTFCTDLAIKLAKKEFGVAVVVTKNSNHYGACQHYTKKIANAGMVG:142
2  GTAWVDGEMLLGAVVGHTFCTDLAIKLAKKEFGVAVVVTKNSNHYGACQHYTKKIANAGMVG:142
3  STAWVDGEMLLGAVVGHTFCTDLAIVEKAKEFGIGWVVCRESNHYGAGWYADFACRNLVG:148
4  GTAWVDGEMLLGAVVGHTFCTDLAIEKAKNAGIGWVVAKGSNHYGAGWYALRAMKKGMLG:180

     190     200     210     220     230     240
1  MSFTNTSPIMFPCRSSEIGLGTNPLSCCVNSEKTGDSFLDMATTTVALGKVELADCRGK:202
2  MSFTNTSPIMFPCRSSEIGLGTNPLSCCANSEKTGDSFLDMATTTVALGKVELANCRGK:202
3  MAFNTNTSPCVFPTGSRKSLGSEPI.CMAAPGMEGDSFLDMASTTVAYGKIEVVDRKGE:207
4  MSMTHNTSPISFPTRSAPVALGTNPI.SLAAPGTGDDSEFLDMASTTVAILGKVELAARK.E:238

     250     260     270     280     290     300
1  TQIPSTWGADSKGNPSTDTQVVLHGGGLLPGLGIEETGSYKGTGLSMMGELFCGILAGSS:262
2  TQIPSAWGADSKGNPSTDTQVVLHGGGLLPGLGIEETGSYKGTGLSMMGELFCGILAGSS:262
3  TYIPGSWGADKNGDETHNPKEVLDGGGLQPLGGSEITGGYKGTGLCMMVEVLCGIMGCSA:267
4  NPVPLSWGVGEGGKETDPTKVLVYGGGLLPGLGVEVSGGYKGYGLSSMIEIFCGILAGAH:298

     310     320     330     340     350     360
1  FGKEVRLWGQSHKAADNGQCFVAIDQECFAPGFAPRLQQLDETRELKPISEEEKPVLPVG:322
2  FGKEVRLWGQSHKAADNGQCFVAIDQECFAPGFAPRLQQLDETRELKPISEEEKPVLPVG:322
3  FGKEIRQWQTTSKTADLGQCFVAIDPECFAPGFSERLQQLDETRELKPINPSRPPQVPVG:327
4  WGFHVVRKWMSTKSEADLGQCFVAIDPEAFAPGFADRLQDEMOTMRALETSSPSFKVEVAG:358

     370     380     390     400
1  DPERMNTTEYSQKAGGLVYQEGQIKALEELATKCDVQMFSYKRLK.:366
2  DPERMNTTEYSQKAGGLVYQEGQIKALEELATKCDVQMFSYKRLK.:366
3  DPERAHNMCDLGGIVYKKKQLDHLKLNADRLGVIMRLVDEKPPQ:372
4  DMERRHEALVEQLGGIPYHKNQITTFVNDIAAKLGVKTVDLVQ....:400

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FIGURE 3

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